

## BOOK REVIEW

**Gene flow between crops and their wild relatives**

Meike S. Andersson and M. Carmen de Vicente 2010. The Johns Hopkins University Press

Gene flow from domesticated plants to free-growing relatives was a rather trivial issue before the advent of transgenic crops. Gene flow into crops was relatively more important, especially to plant breeders trying to introduce new genes in a crop, or to breeders and seed growers wanting to ensure the genetic purity of a cultivar. Genes can now be transferred from bacteria, or potentially any plant or animal species into crops and so, crop to weed gene flow is not so trivial anymore. What if these transgenes can persist in the environment? Anyone interested in this biosafety issue will soon realize that potential gene flow from crops is highly variable depending on the crop species and the presence of wild relatives where the crop is currently cultivated. While information on specific crops abounds, especially in scientific journals, most reviews that include multiple crops are published as regulatory reports and focus on crops grown in developed countries. The main objective of this book was to compile information on relationships between cultivated crops and their wild relatives in order to promote the conservation and utilization of crop genetic resources. Therefore, crops uncommon in developed countries but grown in areas of high biodiversity are included. Andersson and de Vicente, have worked and collaborated with multiple institutions and scientists around the world (Costa Rica, Germany, Colombia, USA and Italy, to name a few) to write this review. It is a good reference source, especially for regulators and policymakers, but also of interest to breeders, plant evolutionists, ecologists, conservationists, agronomists and botanists. The book allows the rapid assessment of gene flow potential by crop (each chapter from 2 to 22 focuses on a single crop) and by geographical location (world maps are presented at the end of the book). Each crop is introduced with a nice picture of its inflorescence. Chapters are in alphabetical order according to crop common name. Crop names are also found at the bottom right of odd pages, providing a simple index that allows rapid consultation.

Chapter one outlines the importance of crop diversity and gene flow, as more and more genetically modified (GM) crops are planted. The authors define terms such as: gene flow, hybridization, introgression and ecological effects of introgression. Chapter two essentially describes the methodology for selecting and gathering the information.

The method used for the modeled likelihood of introgression for each crop (the innovative world maps) is described with more details on pages 549–560. Subsequent chapters each focus on a single crop selected according to three criteria (i) world production area, (ii) advances in GM technology and (iii) relative contribution to food security. For each crop, the number of domesticated species is mentioned along with the reason for selecting one or two species. The center(s) of origin and diversity are listed, followed by information on flowering, pollen biology, reproduction, seed dispersal and dormancy, persistence, weediness/invasiveness, crop wild relatives (also listed in a Table) and hybridization. Finally, there is information on bridge species, pollen flow (sometimes illustrated as a figure presenting outcrossing as a function of distance), isolation distances, state of the GM technology for the crop, agronomic management recommendations to minimize gene flow, crop production area, research gaps and conclusions.

The first chapter provides a good introduction to the subject although some statements are over simplistic. For example, stating that ‘seed dormancy of some GM canola is significantly higher than non-GM controls under some field conditions (Linder. 1998. Ecological Applications 8:1180–1195)’ without mentioning that the GM trait modifies oil composition, is misleading. Oil composition can potentially alter seed dormancy since seed oils are sources of energy prior to the initiation of photosynthesis (*in* Linder and Smith. 1995. Ecological Applications 5:1056–1068, in the references).

I wish the method used to rank and select the twenty crops was described or some explanation given as to why sugarcane (*Saccharum* spp.) [24 million ha (M ha) in 2008], sunflower (*Helianthus annuus*) (25 M ha in 2008) (<http://faostat.fao.org/>) or all forage crops were left out in favor of cotton (*Gossypium hirsutum* and *G. barbadense*) (33 M ha, advances in GM technology, but how much does it contribute to food security?), pigeon peas (*Cajanus cajan*) (4.6 M ha, no commercial GM production) or finger millet (*Eleusine coracana*) (4 M ha, no transformation protocols). I salute the inclusion of food crops produced essentially in India (pigeon peas) and Africa (finger millet), but expected to find sugarcane or alfalfa (*Medicago sativa*). Perhaps it should have been specified

that high biodiversity in the center of origin of the crop was also decisive in crop selection, if that is the case.

The wealth of information provided for each crop is sometimes redundant as seed dormancy, persistence of volunteers and weediness are often interrelated, but I trust, most of the important information has been covered (at least from my knowledge of a few crops). Also, the source for agronomic management recommendations is unclear as none are provided for most crops (13/20) and few to no references are listed to support the four to seven recommendations. Finally, it is difficult to assess the accuracy of the maps showing the modeled likelihood of introgression since a detailed description of the geographic mapping methodology, which is based on a few known geographical locations of the species and bio-climatic variables, is in preparation (Andersson et al. in prep.) and therefore cannot be consulted. Although I recognize that the maps want to give an indication of the potential gene flow if wild relatives occupy and expand their entire ranges based on bio-climatic requirements, this can easily lead to overestimations as climate is not the only variable limiting species ranges. As a case in point, the *Brassica napus* (canola) and *Triticum aestivum* (wheat) maps essentially suggest that there is moderate to high likelihood of gene flow in cultivated areas across Canada. However, both *B. napus* fields and *Brassica rapa* weeds are infrequent in Southern Ontario, no known wild *Triticum* species exist in Canada (<http://www.inspection.gc.ca/english/plaveg/bio/dir/biodoce.shtml>) and *Aegilops cylindrica* has a very limited distribution in a single province (<http://www.inspection.gc.ca/english/plaveg/invenv/pestrava/aegcyl/aegcylfse.shtml>). That said, I acknowledge that mapping gene flow potential on a world scale is not an easy task and maps will initially be rudimentary. These maps are publicly available on the web (not at the location indicated in the book, but at <http://gisweb.ciat.cgiar.org/geneflow/>) and will possibly be refined as more information becomes available. I had problems trying to map the data provided and, as I do not like to spend time on that type of technical problem, I abandoned the visualization of the web maps.

In spite of the few inevitable minor errors, over simplistic statements, omissions and mismatched references here and there, I learned much more than I could criticize from this 564 page book. For example, I learned that there is little information on the pollen biology of bananas and plantains (*Musa* spp.), that finger millet (*E. coracana*) and wild relatives are among the least analysed crops, that some teosintes (*Zea mays* subspecies and *Zea* spp.) are rare and endangered, that the main constraint for developing transgenic peanuts (*Arachis hypogaea*) is the lack of agronomically useful genes, that some wild relatives of cotton (*Gossipium* spp.) are endemic, that potatoes (*Solanum tuberosum*) have complex hybridization barriers, that the origin of shattercane (*Sorghum bicolor* weed) still awaits clarification and that ants can disperse rice (*Oryza sativa*) seeds.

Having read the entire book, I wish the authors would have included a general conclusion regarding gene flow between crops and their wild relatives. It is important to recognize that most crops have low outcrossing rates, informal seed exchange systems, low seed dormancy and shattering (as a consequence of domestication), wild relatives in their center(s) of origin (since crops come wild plants) and that information on pollen duration and viability is lacking for a number of crop species.

The book certainly achieves its goal to compile available information on relationships between cultivated crops and their wild relatives. As mentioned in the foreword by Norman C. Ellstrand, an authority on gene flow, assembling information for so many crops was undoubtedly a titanic task. All this work generated a solid initial reference book for anyone dealing with, or interested in, the transfer of genes between cultivated and free-growing plants. This book will undoubtedly promote awareness on biodiversity in the context of plant domestication and cultivation.

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